SCORE Search Results Details for Application 10568337 and Search Result 20071129_084935_20071129_084935_us-10-568-337-2.p2n.rni.

Score Home Page | Retrieve Application List | SCORE System Overview | SCORE FAQ | Comments / Suggestions

This page gives you Search Results detail for the Application 10568337 and Search Result 20071129_084935_20071129_084935_us-10-568-337-2.p2n.rni.

Go Back to previous page

GenCore version 6.2.1

OM protein - nucleic search, using frame_plus_p2n model

Run on: November 29, 2007, 08:49:46 ; Search time 836 Seconds
(without alignments)
120.985 Million cell updates/sec

Title: US-10-568-337-2
Perfect score: 124
Sequence: 1 MLRVLHRAASALVMATVIGLAPAVAFA 27

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 5155175 seqs, 1873024446 residues

Total number of hits satisfying chosen parameters: 10310228

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Command line parameters:
-THR=4 -MODEL=frame+_p2n.model -DEV=SOFT
-Q=/abss/ABSSWEB_spool/US10568337/runat_29112007_084935_26715/app_query.fasta_1
-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=p2n.rni -SIMRANGE=0.0005
-MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1
-MATRIX=blosum62 -TRANS=human40.cdi -LIST=1000 -DOCALIGN=200 -THR_SCORE=pct
-THR_MAX=100 -THR_MIN=0 -ALIGN=50 -MODE=LOCAL -OUTFMT=pto -NORM=ext
-HEAPSIZE=0 -MINLEN=0 -MAXLEN=2000000000 -MINDBSEQLEN=1 -HOST=ai1-01
-USER=US10568337_@CGN_1_1_134_@runat_29112007_084935_26715 -NCPU=6 -NO_MMAP
-NEG_SCORES=0 -WAIT -LONGLOG -MINDIST=10 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued_Patents_NA:*
1: /EMC_Celerra_SIDS2/ptodata/1/ina/1_COMB.seq:*
2: /EMC_Celerra_SIDS2/ptodata/1/ina/5_COMB.seq:*
3: /EMC_Celerra_SIDS2/ptodata/1/ina/6A_COMB.seq:*
4: /EMC_Celerra_SIDS2/ptodata/1/ina/6B_COMB.seq:*
5: /EMC_Celerra_SIDS2/ptodata/1/ina/7A_COMB.seq:*
6: /EMC_Celerra_SIDS2/ptodata/1/ina/7B_COMB.seq:*
7: /EMC_Celerra_SIDS2/ptodata/1/ina/H_COMB.seq:*
8: /EMC_Celerra_SIDS2/ptodata/1/ina/PCTUS_COMB.seq:*
9: /EMC_Celerra_SIDS2/ptodata/1/ina/PP_COMB.seq:*
10: /EMC_Celerra_SIDS2/ptodata/1/ina/RE_COMB.seq:*
11: /EMC_Celerra_SIDS2/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	124	100.0	2163	2	US-07-731-157A-1	Sequence 1, Appli
	2	124	100.0	2163	2	US-08-541-780-1	Sequence 1, Appli
	3	55	44.4	36	2	US-07-731-157A-11	Sequence 11, Appl
	4	55	44.4	36	2	US-08-541-780-11	Sequence 11, Appl
c	5	54	43.5	531	5	US-10-703-032-95089	Sequence 95089, A
c	6	54	43.5	539	5	US-10-703-032-91504	Sequence 91504, A
c	7	54	43.5	588	5	US-10-703-032-94706	Sequence 94706, A
c	8	53	42.7	419	5	US-10-703-032-49153	Sequence 49153, A
c	9	52.5	42.3	378	5	US-10-703-032-89469	Sequence 89469, A
c	10	52.5	42.3	396	5	US-10-703-032-98346	Sequence 98346, A
c	11	52.5	42.3	418	5	US-10-703-032-98096	Sequence 98096, A
c	12	52.5	42.3	422	5	US-10-703-032-96699	Sequence 96699, A
c	13	52.5	42.3	425	5	US-10-703-032-97933	Sequence 97933, A
c	14	52.5	42.3	428	5	US-10-703-032-80385	Sequence 80385, A
c	15	52.5	42.3	433	5	US-10-703-032-80412	Sequence 80412, A
c	16	52.5	42.3	438	5	US-10-703-032-49995	Sequence 49995, A
c	17	52.5	42.3	473	5	US-10-703-032-92026	Sequence 92026, A
c	18	52.5	42.3	475	5	US-10-703-032-55226	Sequence 55226, A

<!--StartFragment--> ALIGNMENTS

```
RESULT 1
US-07-731-157A-1
; Sequence 1, Application US/07731157A
; Patent No. 5457032
;  GENERAL INFORMATION:
;    APPLICANT:  Quax, Wilhelmus J.
;    APPLICANT:  Misset, Onno
;    APPLICANT:  Van der Laan, Jan M.
;    APPLICANT:  Lenting, Herman B.M.
;    TITLE OF INVENTION:  Mutated beta-lactam acylase genes
;    NUMBER OF SEQUENCES:  50
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  COOLEY GODWARD CASTRO HUDDLESON & TATUM
;      STREET:  FIVE PALO ALTO SQUARE, 4TH FLOOR
;      CITY:  PALO ALTO
;      STATE:  CALIFORNIA
;      COUNTRY:  USA
;      ZIP:  94306
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25 (EPO)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/731,157A
;      FILING DATE:  19910509
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  EP 90200962
;      FILING DATE:  18-APR-1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  RAE-VENTER PH.D., BARBARA
;      REGISTRATION NUMBER:  32,750
;      REFERENCE/DOCKET NUMBER:  GBRO-027/00US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-494-7622
;      TELEFAX:  415-857-0663
;      TELEX:  380816 COOLEY PA
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2163 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Pseudomonas species
;      STRAIN:  SY77
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..2163
;      IDENTIFICATION METHOD:  experimental
;      OTHER INFORMATION:  /codon_start= 1
;      OTHER INFORMATION:  /product= "Glutaryl-Cef acylase"
;      OTHER INFORMATION:  /evidence= EXPERIMENTAL
;    FEATURE:
;      NAME/KEY:  sig_peptide
```

```
;      LOCATION:  1..87
;    FEATURE:
;      NAME/KEY:  mat_peptide
;      LOCATION:  88..594
;      OTHER INFORMATION:  /product= "glutaryl-cef acylase"
;      OTHER INFORMATION:  /label= alfa-subunit
;    FEATURE:
;      NAME/KEY:  mat_peptide
;      LOCATION:  595..2163
;      OTHER INFORMATION:  /product= "glutaryl-cef acylase"
;      OTHER INFORMATION:  /label= beta-subunit
US-07-731-157A-1

Alignment Scores:
Pred. No.:              3.68e-11       Length:         2163
Score:                  124.00         Matches:        27
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            100.0%         Indels:         0
DB:                     2              Gaps:           0

US-10-568-337-2 (1-27) x US-07-731-157A-1 (1-2163)

Qy          1 MetLeuArgValLeuHisArgAlaAlaSerAlaLeuValMetAlaThrValIleGlyLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGCTGAGAGTTCTGCACCGGGCGGCGTCCGCCTTGGTTATGGCGACTGTGATCGGCCTT 60

Qy         21 AlaProAlaValAlaPheAla 27
              |||||||||||||||||||||
Db         61 GCGCCCGCCGTCGCCTTTGCG 81

RESULT 2
US-08-541-780-1
; Sequence 1, Application US/08541780
; Patent No. 5935831
;  GENERAL INFORMATION:
;    APPLICANT:  Quax, Wilhelmus J.
;    APPLICANT:  Misset, Onno
;    APPLICANT:  Van der Laan, Jan M.
;    APPLICANT:  Lenting, Herman B.M.
;    TITLE OF INVENTION:  Mutated beta-lactam acylase genes
;    NUMBER OF SEQUENCES:  50
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  COOLEY GODWARD CASTRO HUDDLESON & TATUM
;      STREET:  FIVE PALO ALTO SQUARE, 4TH FLOOR
;      CITY:  PALO ALTO
;      STATE:  CALIFORNIA
;      COUNTRY:  USA
;      ZIP:  94306
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25 (EPO)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/541,780
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/731,157
;      FILING DATE:
```

```
;       APPLICATION NUMBER:  EP 90200962
;       FILING DATE:  18-APR-1990
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  RAE-VENTER PH.D., BARBARA
;       REGISTRATION NUMBER:  32,750
;       REFERENCE/DOCKET NUMBER:  GBRO-027/00US
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  415-494-7622
;       TELEFAX:  415-857-0663
;       TELEX:  380816 COOLEY PA
;   INFORMATION FOR SEQ ID NO:  1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  2163 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  double
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA (genomic)
;     HYPOTHETICAL:  NO
;     ANTI-SENSE:  NO
;     ORIGINAL SOURCE:
;       ORGANISM:  Pseudomonas species
;       STRAIN:  SY77
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  1..2163
;       IDENTIFICATION METHOD:  experimental
;       OTHER INFORMATION:  /codon_start= 1
;       OTHER INFORMATION:  /product= "Glutaryl-Cef acylase"
;       OTHER INFORMATION:  /evidence= EXPERIMENTAL
;     FEATURE:
;       NAME/KEY:  sig_peptide
;       LOCATION:  1..87
;     FEATURE:
;       NAME/KEY:  mat_peptide
;       LOCATION:  88..594
;       OTHER INFORMATION:  /product= "glutaryl-cef acylase"
;       OTHER INFORMATION:  /label= alfa-subunit
;     FEATURE:
;       NAME/KEY:  mat_peptide
;       LOCATION:  595..2163
;       OTHER INFORMATION:  /product= "glutaryl-cef acylase"
;       OTHER INFORMATION:  /label= beta-subunit
US-08-541-780-1

Alignment Scores:
Pred. No.:              3.68e-11        Length:         2163
Score:                  124.00          Matches:        27
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     2               Gaps:           0

US-10-568-337-2 (1-27) x US-08-541-780-1 (1-2163)

Qy          1 MetLeuArgValLeuHisArgAlaAlaSerAlaLeuValMetAlaThrValIleGlyLeu 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGCTGAGAGTTCTGCACCGGGCGGCGTCCGCCTTGGTTATGGCGACTGTGATCGGCCTT 60

Qy         21 AlaProAlaValAlaPheAla 27
              |||||||||||||||||||||
Db         61 GCGCCCGCCGTCGCCTTTGCG 81
```

<!--EndFragment-->

SCORE Search Results Details for Application 10568337 and Search Result 20071128_153802_us-10-568-337-5.rng.

Score Home Page | Retrieve Application List | SCORE System Overview | SCORE FAQ | Comments / Suggestions

This page gives you Search Results detail for the Application 10568337 and Search Result 20071128_153802_us-10-568-337-5.rng.

Go Back to previous page

```
                        GenCore version 6.2.1
                  Copyright (c) 1993 - 2007  Biocceleration Ltd.


OM nucleic - nucleic search, using sw model

Run on:          November 29, 2007, 00:22:26 ; Search time 646 Seconds
                                             (without alignments)
                                             1147.147 Million cell updates/sec

Title:           US-10-568-337-5
Perfect score:   100
Sequence:        1 atcctggttcgtacgcgccg.........ctgggtgagaggggaaatcc 100

Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        5620219 seqs, 3705283702 residues

Total number of hits satisfying chosen parameters:      11240438

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :        N_Geneseq_200701:*
                 1:  geneseqn1980s:*
                 2:  geneseqn1990s:*
                 3:  geneseqn2000s:*
                 4:  geneseqn2001as:*
                 5:  geneseqn2001bs:*
                 6:  geneseqn2002as:*
                 7:  geneseqn2002bs:*
                 8:  geneseqn2003as:*
                 9:  geneseqn2003bs:*
                 10:  geneseqn2003cs:*
                 11:  geneseqn2003ds:*
                 12:  geneseqn2004as:*
                 13:  geneseqn2004bs:*
                 14:  geneseqn2005s:*
                 15:  geneseqn2006s:*
```

16: geneseqn2007s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	100	100.0	100	14	ADY34485	Ady34485 Pseudomon
	2	100	100.0	209	14	ADY34486	Ady34486 Pseudomon
	3	100	100.0	315	14	ADY34493	Ady34493 Pseudomon
	4	100	100.0	315	14	ADX70106	Adx70106 Recombina
	5	100	100.0	807	14	ADY34499	Ady34499 Human int
	6	100	100.0	807	14	ADX70111	Adx70111 Recombina
	7	94.8	94.8	101	4	AAH27732	Aah27732 GL7ACA (a
	8	94.8	94.8	101	5	AAH27740	Aah27740 Gl-7ACA r
	9	93.2	93.2	2482	4	AAI64747	Aai64747 Pseudomon
c	10	30.6	30.6	489	12	ADQ21106	Adq21106 Human sof
c	11	30.6	30.6	560	6	ABK35222	Abk35222 Human cDN
c	12	30.6	30.6	2222	10	ADL25751	Adl25751 Human can
c	13	30.6	30.6	2222	10	ADL25753	Adl25753 Human can
c	14	30.6	30.6	4369	12	ADQ25015	Adq25015 Human sof
c	15	29.6	29.6	1032	5	AAH74579	Aah74579 Nucleotid
	16	29	29.0	110000	4	AAI99682_19	Continuation (20 o
	17	29	29.0	110000	4	AAI99683_19	Continuation (20 o
c	18	28.6	28.6	46235	15	AEF73891	Aef73891 Human cor
c	19	28.6	28.6	49999	2	AAZ23903	Aaz23903 Human LOB
	20	28.2	28.2	706	2	ADR02076	Adr02076 A. gossyp
	21	28.2	28.2	1329	8	ACA19622	Aca19622 Prokaryot
c	22	27.6	27.6	346	3	AAA31766	Aaa31766 Plant mic
c	23	27.6	27.6	438	3	AAA31518	Aaa31518 Plant mic
	24	27.4	27.4	193303	12	ADF13122	Adf13122 Hypermeth
	25	27.4	27.4	193303	12	ADF13115	Adf13115 Hypermeth
	26	27.4	27.4	193303	12	ADI37268	Adi37268 Hypermeth
	27	27.4	27.4	193303	12	ADI37261	Adi37261 Hypermeth
c	28	27.2	27.2	5286	4	ABL05391	Abl05391 Drosophil
c	29	27.2	27.2	8303	4	ABL05390	Abl05390 Drosophil
	30	27	27.0	1260	11	ACL26209	Acl26209 Rice abio
c	31	27	27.0	1387	13	ADX62879	Adx62879 Plant ful
	32	26.8	26.8	825	14	ACL70964	Acl70964 M. xanthu
c	33	26.8	26.8	2955	13	ADO84038	Ado84038 Plant ful
	34	26.8	26.8	10916	14	ACL64594	Acl64594 M. xanthu
c	35	26.8	26.8	33126	12	ADQ97546	Adq97546 Mouse can
c	36	26.6	26.6	441	11	ABD05702	Abd05702 Pseudomon
c	37	26.6	26.6	1317	11	ABD05624	Abd05624 Pseudomon
	38	26.6	26.6	1398	11	ABD06048	Abd06048 Pseudomon
c	39	26.6	26.6	3406	2	AAX20567	Aax20567 Polynucle
	40	26.4	26.4	494	14	ACL55838	Acl55838 Human col
	41	26.4	26.4	500	6	ABL65055	Abl65055 Lung canc
c	42	26.4	26.4	1441	11	AEA90319	Aea90319 Human NOV
c	43	26.4	26.4	2331	6	ABK34734	Abk34734 Human cDN
	44	26.4	26.4	3707	2	AAQ82792	Aaq82792 TRK1 gene
	45	26.4	26.4	3708	5	AAH21448	Aah21448 S. cerevi

<!--StartFragment-->RESULT 4
ADX70106
ID   ADX70106 standard; DNA; 315 BP.
XX
AC   ADX70106;
XX
DT   05-MAY-2005 (first entry)
XX
DE   Recombinant protein preparation method-related gaclss gene region SeqID8.
XX
KW   fermentation; expression; recombinant protein; protein production;
KW   interferon alpha 2; gene; ds.
XX
OS   Brevundimonas diminuta.
XX
PN   WO2005017174-A2.
XX
PD   24-FEB-2005.
XX
PF   12-AUG-2004; 2004WO-EP009055.
XX
PR   13-AUG-2003; 2003US-0494915P.
XX
PA   (SANO) SANDOZ AG.
XX
PI   Stempfer G, Alliger P, Palma N;
XX
DR   WPI; 2005-182386/19.
XX
PT   Preparing recombinant polypeptides of interest, for producing large
PT   variety of polypeptides of interest, by fermenting prokaryotic host cell
PT   comprising a periplasm transformed with a recombinant expression system.
XX
PS   Example 1; SEQ ID NO 8; 29pp; English.
XX
CC   This invention relates to a novel method of preparing a recombinant
CC   polypeptide of interest which comprises fermenting a prokaryotic host
CC   cell comprising a periplasm transformed with a recombinant expression
CC   system capable of bringing secretion of a polypeptide of interest into
CC   the periplasm of the host cell and extracting the polypeptide of interest
CC   from the periplasm. The method is useful for preparing a wide variety of
CC   recombinant polypeptides of interest such as human interferon alpha 2.
CC   The present sequence is that of a region of the B diminuta gaclss gene
CC   which was used in the exemplification of the invention.
XX
SQ   Sequence 315 BP; 55 A; 86 C; 113 G; 61 T; 0 U; 0 Other;

  Query Match   100.0%; Score 100; DB 14; Length 315;
  Best Local Similarity   100.0%; Pred. No. 6.9e-23;
  Matches 100; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 ATCCTGGTTCGTACGCGCCGCCTACAAGTGGTGATCTAGGGGAACGTTCCGGGGGCGTCG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   116 ATCCTGGTTCGTACGCGCCGCCTACAAGTGGTGATCTAGGGGAACGTTCCGGGGGCGTCG 175

Qy   61 CTGCAACGGCGTCTCCGGATCTGGGTGAGAGGGGAAATCC 100
              |||||||||||||||||||||||||||||||||||||||||
Db   176 CTGCAACGGCGTCTCCGGATCTGGGTGAGAGGGGAAATCC 215

RESULT 5

```
ADY34499
ID   ADY34499 standard; cDNA; 807 BP.
XX
AC   ADY34499;
XX
DT   05-MAY-2005  (first entry)
XX
DE   Human interferon-alpha 2B expression construct.
XX
KW   Recombinant protein; interferon-alpha; mutant; gac gene; signal peptide;
KW   gene; ss.
XX
OS   Homo sapiens.
OS   Brevundimonas diminuta.
OS   Chimeric.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             210. .788
FT                   /*tag=  b
FT   sig_peptide     210. .290
FT                   /*tag=  a
FT                   /note= "Gac gene signal sequence"
FT   mat_peptide     291. .785
FT                   /*tag=  c
FT                   /product= "Human mature interferon-alpha 2B"
XX
PN   WO2005017162-A2.
XX
PD   24-FEB-2005.
XX
PF   12-AUG-2004; 2004WO-EP009067.
XX
PR   13-AUG-2003; 2003US-0494914P.
XX
PA   (SANO ) SANDOZ AG.
XX
PI   Windisch J,  Schoergendorfer K,  Palma N,  Knauseder F,  Boehling H;
XX
DR   WPI; 2005-182378/19.
DR   P-PSDB; ADY34498.
XX
PT   New expression vector comprising a polynucleotide encoding a fusion
PT   protein comprising the signal sequence of the gac gene of Pseudomonas
PT   diminuta and a polypeptide other than gac, useful for producing
PT   polypeptides.
XX
PS   Example 1; SEQ ID NO 19; 39pp; English.
XX
CC   The invention provides a process for the efficient and direct production
CC   of a mature recombinant polypeptide in a prokaryotic host cell. A claimed
CC   expression vector comprises a polynucleotide encoding a fusion protein
CC   consisting of the signal sequence ADY34482 of the glutaryl 7-
CC   aminocephalosporic acid acylase (gac) gene of Pseudomonas diminuta and
CC   the polypeptide of interest. A prokaryotic host cell transformed with the
CC   vector is cultured under conditions which cause expression of the
CC   polynucleotide. Upon formation of the fusion protein, the signal sequence
CC   is cleaved off and the polypeptide of interest is released into the
CC   periplasm of the host cell. The expression vector is a plasmid,
CC   preferably a high copy plasmid. The vector further comprises a
CC   polynucleotide comprising the promoter region and the ribosomal binding
```

CC site ADY34485 or ADY34486 of the gac gene of P. diminuta. The culturing
CC is performed as a multi-stage fermentation process comprising a shake-
CC flask step, optionally a pre-culture step, and a main culture step. The
CC main culture step is performed in a culture medium comprising a substrate
CC for more than 90% of the cultivation time at a substrate concentration
CC lower that the saturation constant of the substrate, accompanied by high
CC levels of dissolved oxygen concentration, and further accompanied by a
CC steadily decreasing specific growth rate of the bacterial host cells, the
CC process being performed at a temperature that is lower than the optimum
CC temperature for growth of the host cell. The substrate is glycerol or a
CC carbohydrate, preferably glucose. The process is favorably used for the
CC production of recombinant human interferon-alpha 2B in Escherichia coli.
CC The present sequence is that of an expression construct for recombinant
CC production of human mature interferon-alpha 2B in E. coli. It comprises
CC the P. diminuta signal sequence, promoter and ribosome binding site, and
CC the coding sequence ADY34481 for interferon-alpha 2B in which codons have
CC been modified to improve expression. The expression construct was
CC obtained by a combination of chemical synthesis and PCR amplification.
XX
SQ Sequence 807 BP; 177 A; 215 C; 227 G; 188 T; 0 U; 0 Other;

Query Match 100.0%; Score 100; DB 14; Length 807;
Best Local Similarity 100.0%; Pred. No. 8.1e-23;
Matches 100; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 ATCCTGGTTCGTACGCGCCGCCTACAAGTGGTGATCTAGGGGAACGTTCCGGGGGCGTCG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        110 ATCCTGGTTCGTACGCGCCGCCTACAAGTGGTGATCTAGGGGAACGTTCCGGGGGCGTCG 169

Qy         61 CTGCAACGGCGTCTCCGGATCTGGGTGAGAGGGGAAATCC 100
              |||||||||||||||||||||||||||||||||||||||||
Db        170 CTGCAACGGCGTCTCCGGATCTGGGTGAGAGGGGAAATCC 209
```

<!--EndFragment-->